

Figure 1

3631 GTTGGCTTATCCCTGGAACTGCTGCTTATCTGGGCTTTTCTGCTAGATGTGGGCGTGTTTGGAGGCTGTACTATATGAAGCTGCAATATACTGTGAGCTGTGATTGGGGAACACCAATG
3751 CAGAGCTAATCTCAGGCACTAAGCAAGCACTCAAGAAACATGTTAAATTAACTGCTCTCTCTTACAGTACTTCAAATACAAAAGTGAATGAATGCCATTGCAATTGTACTTCTT

[illegible]

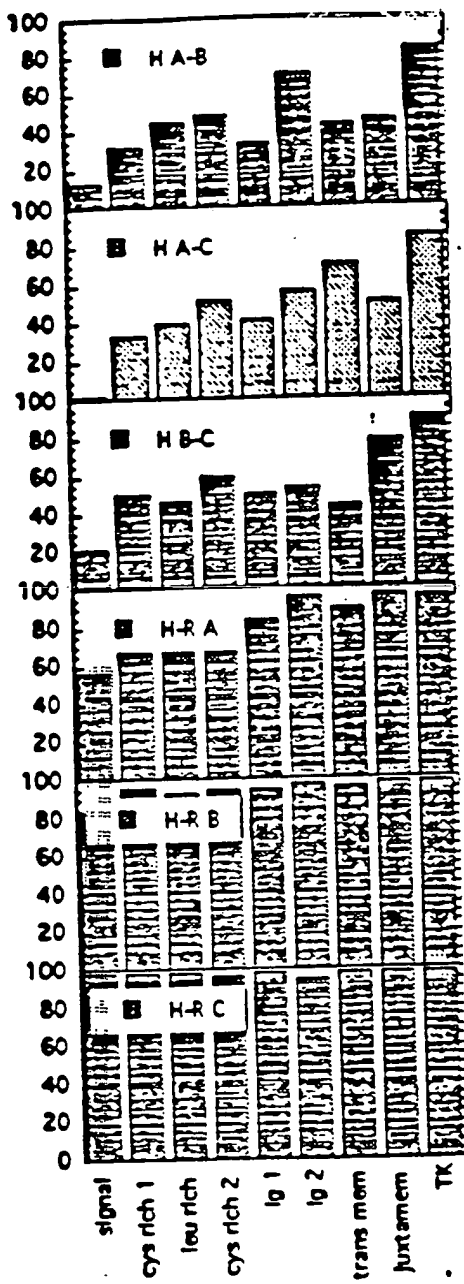


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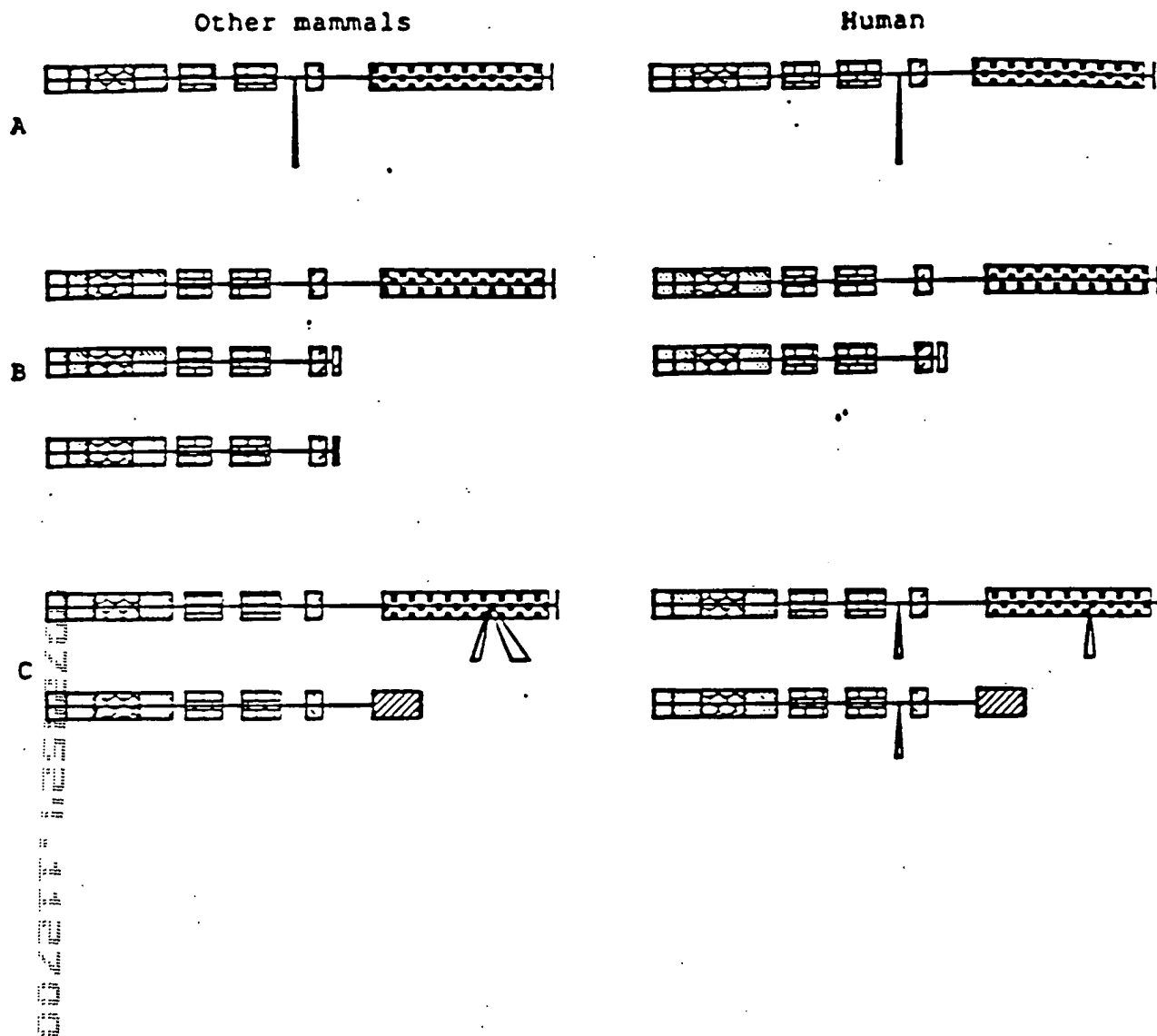
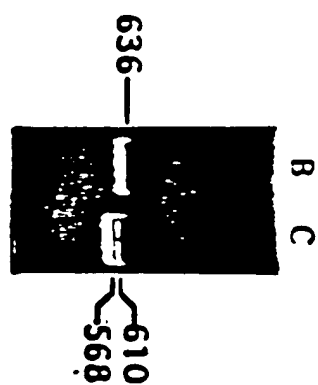


Figure 5



00724500-44200

Figure 6

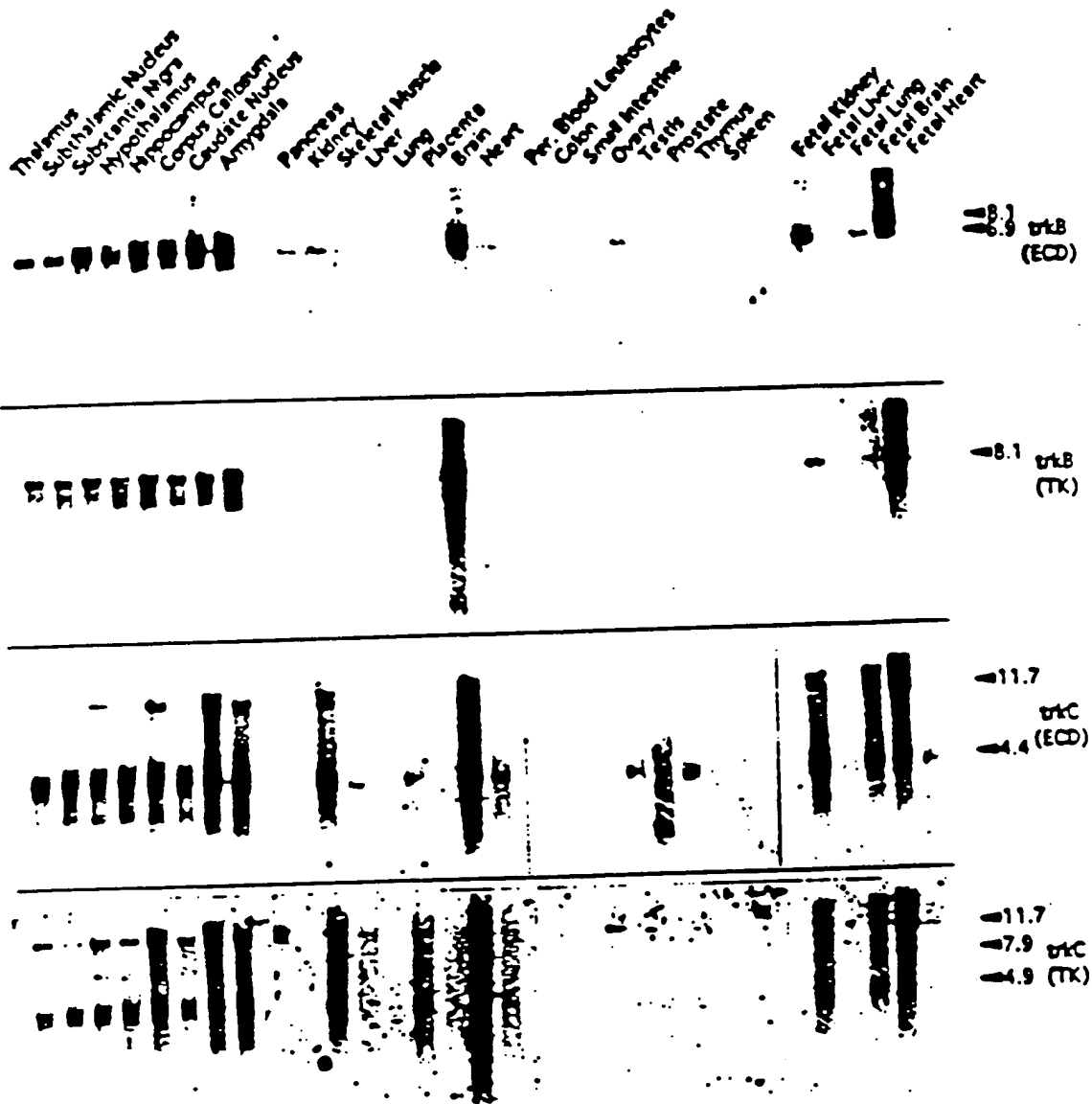
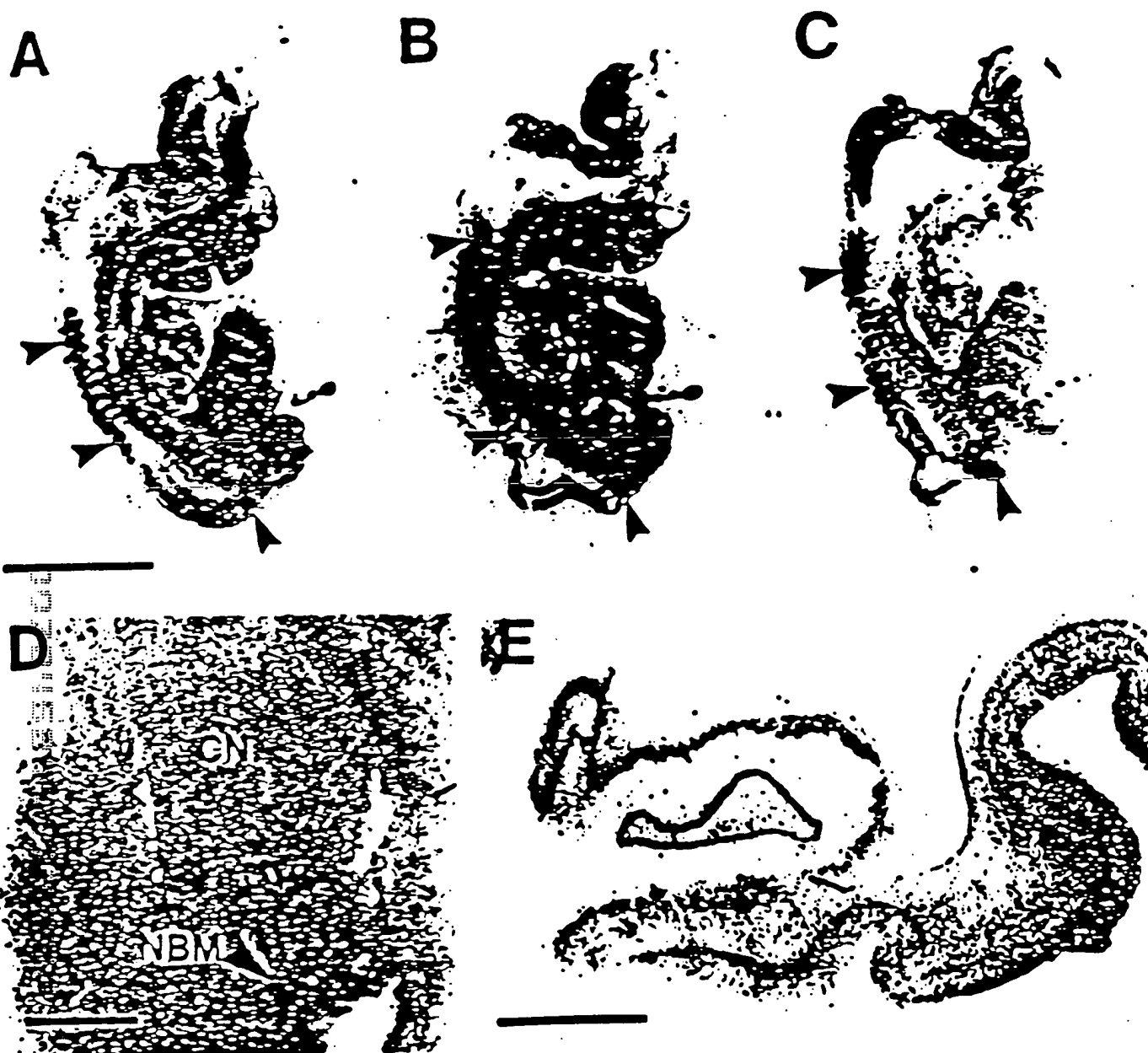


Figure 7



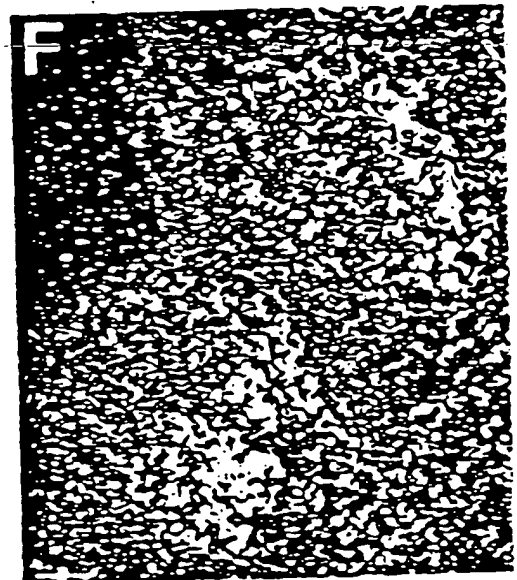
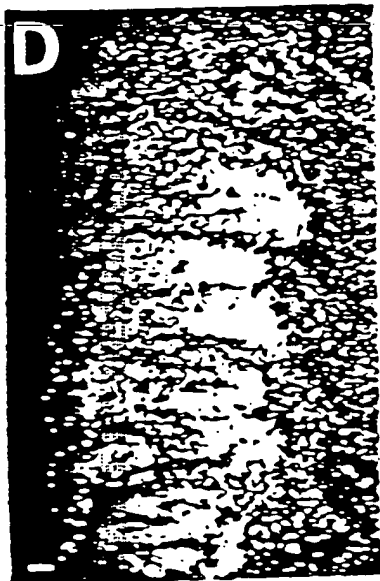
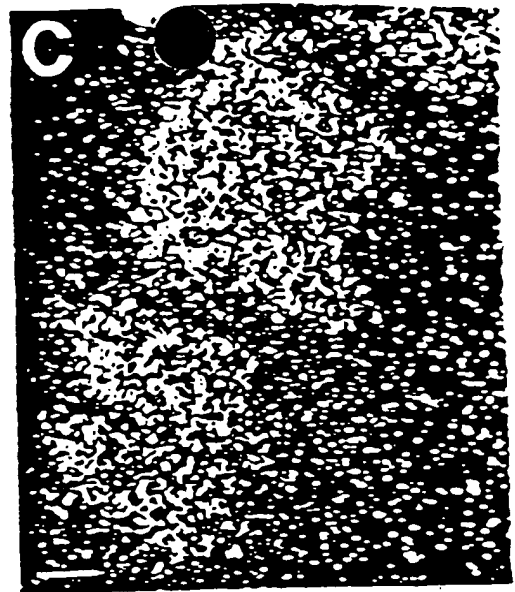
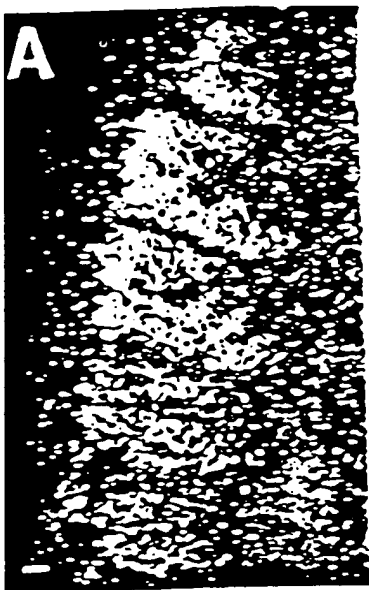


Figure 8

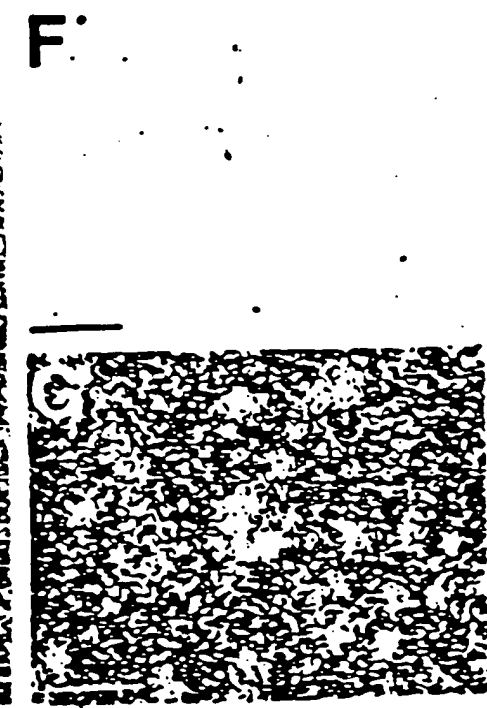
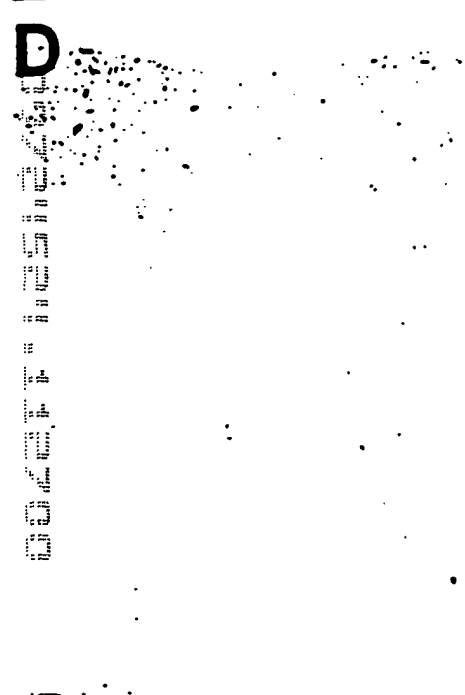
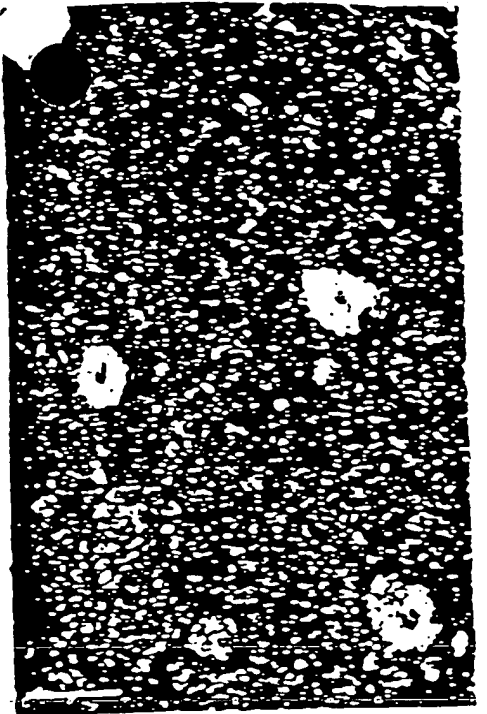
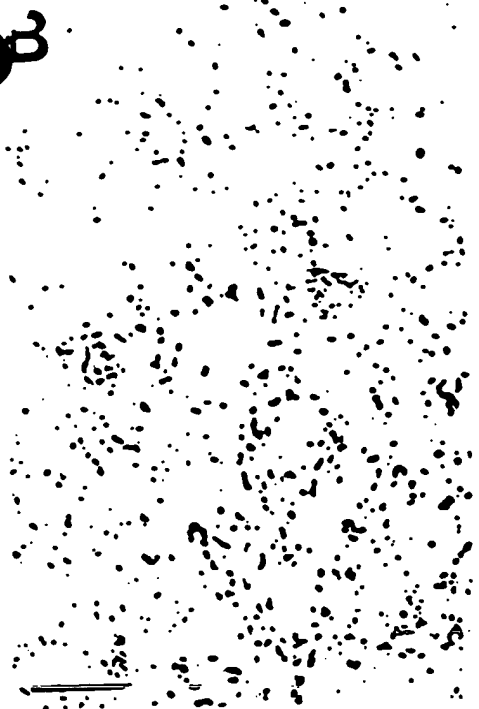
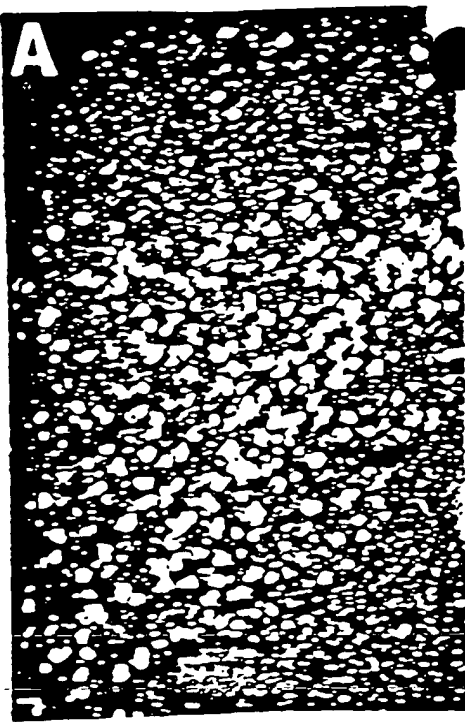


Figure 9

Figure 10

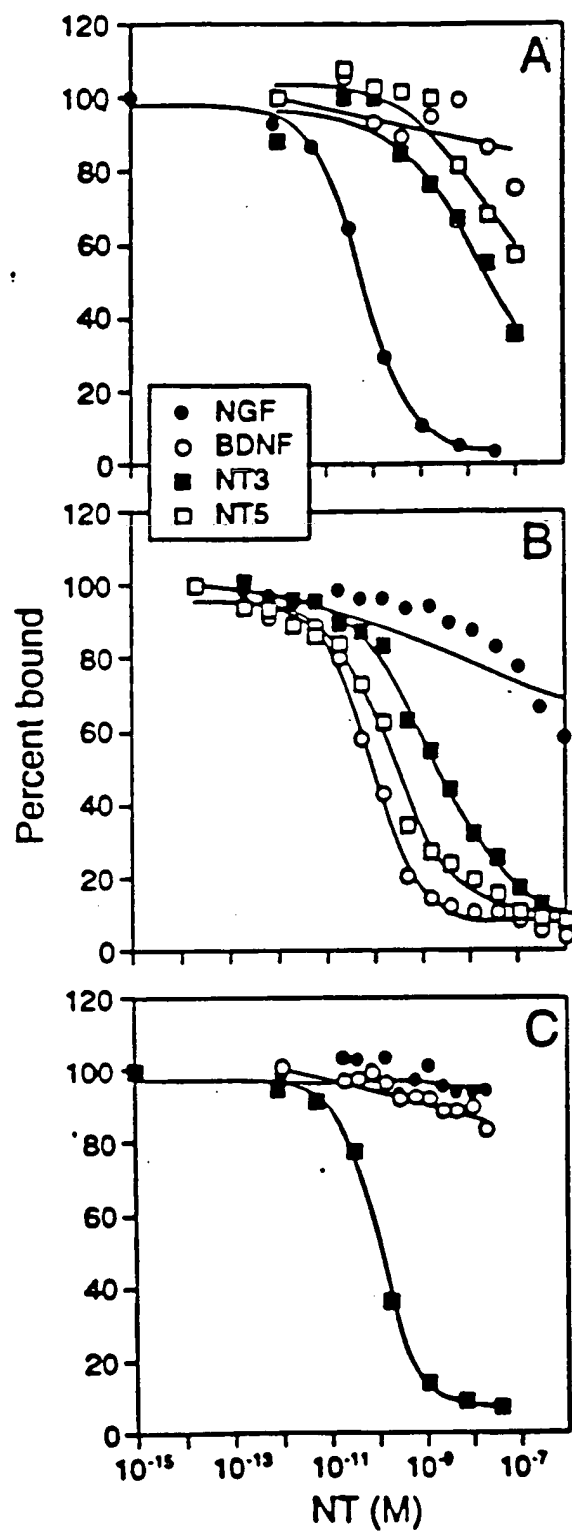


Figure 11

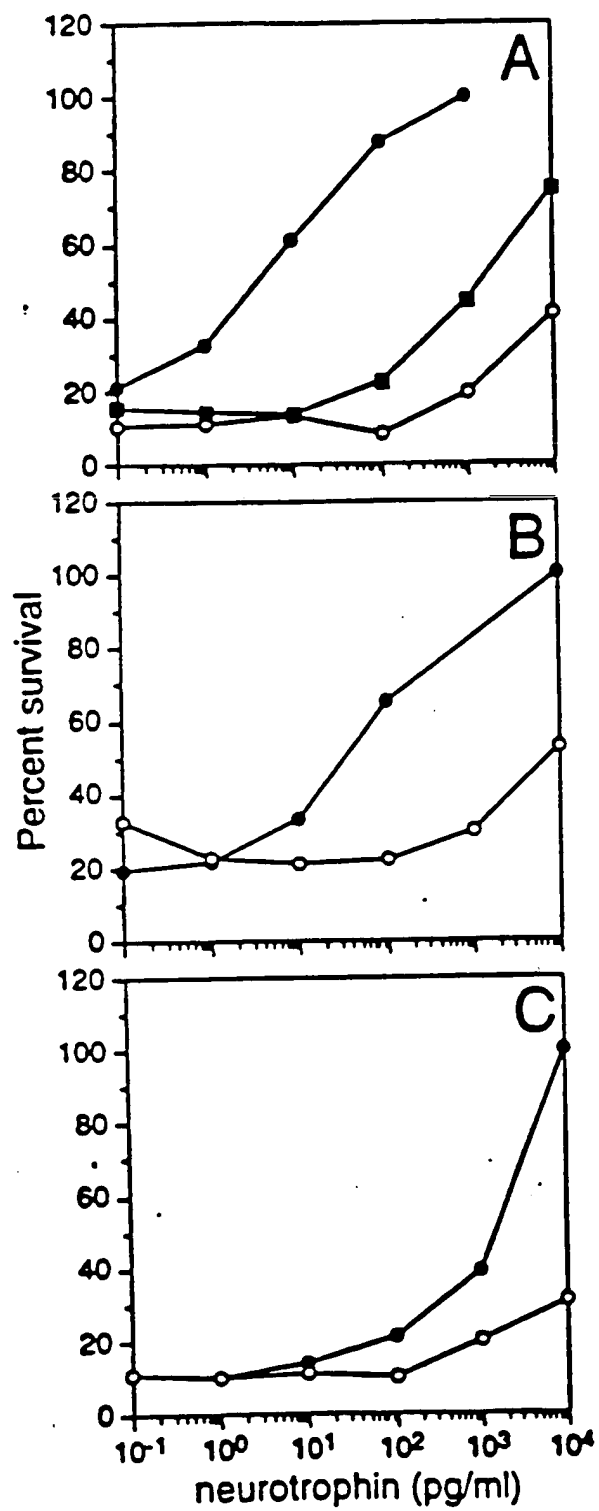


Figure 12

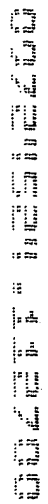
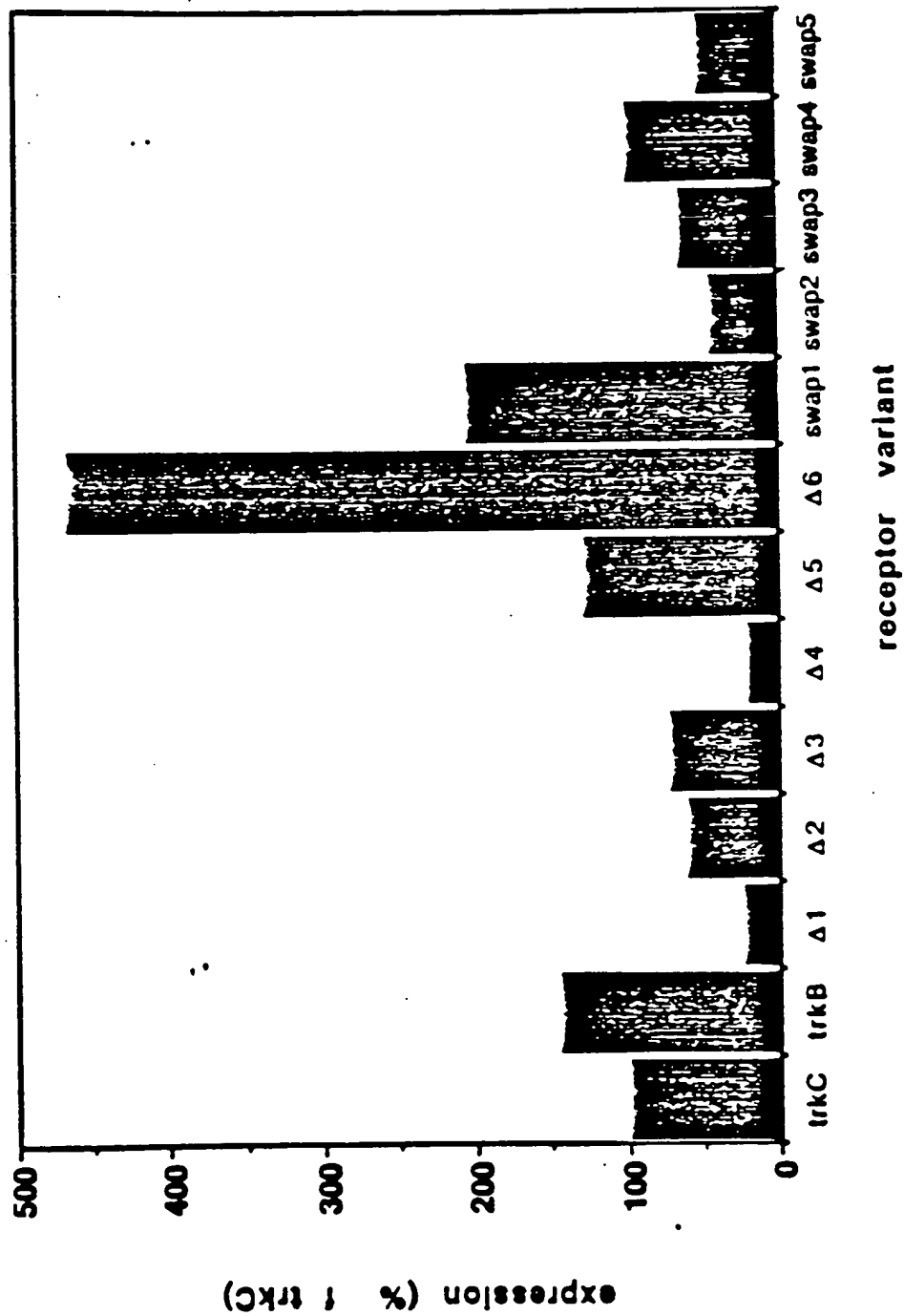


Figure 13

Expression of trkC-Ig variants



WYI m872

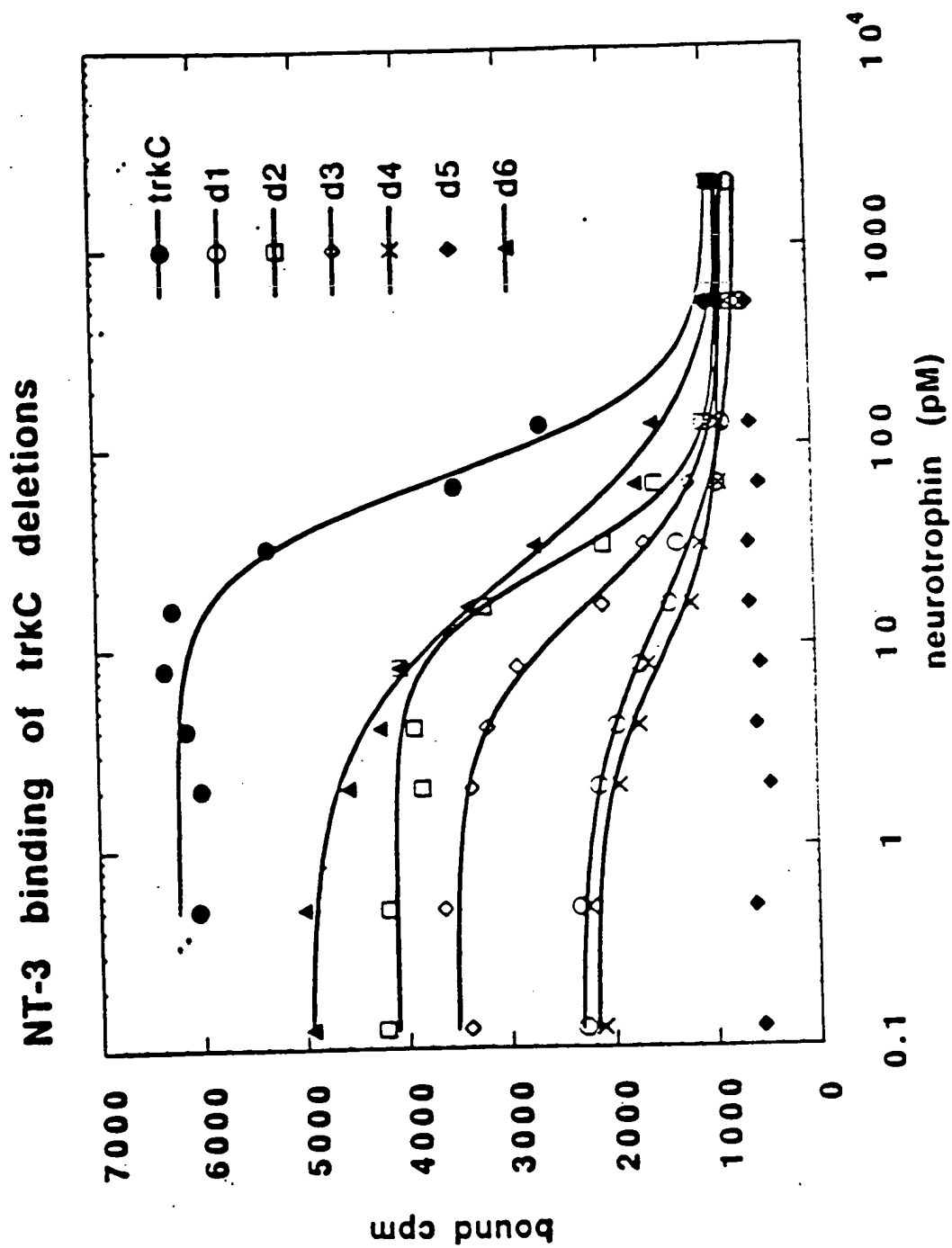


Figure 14B

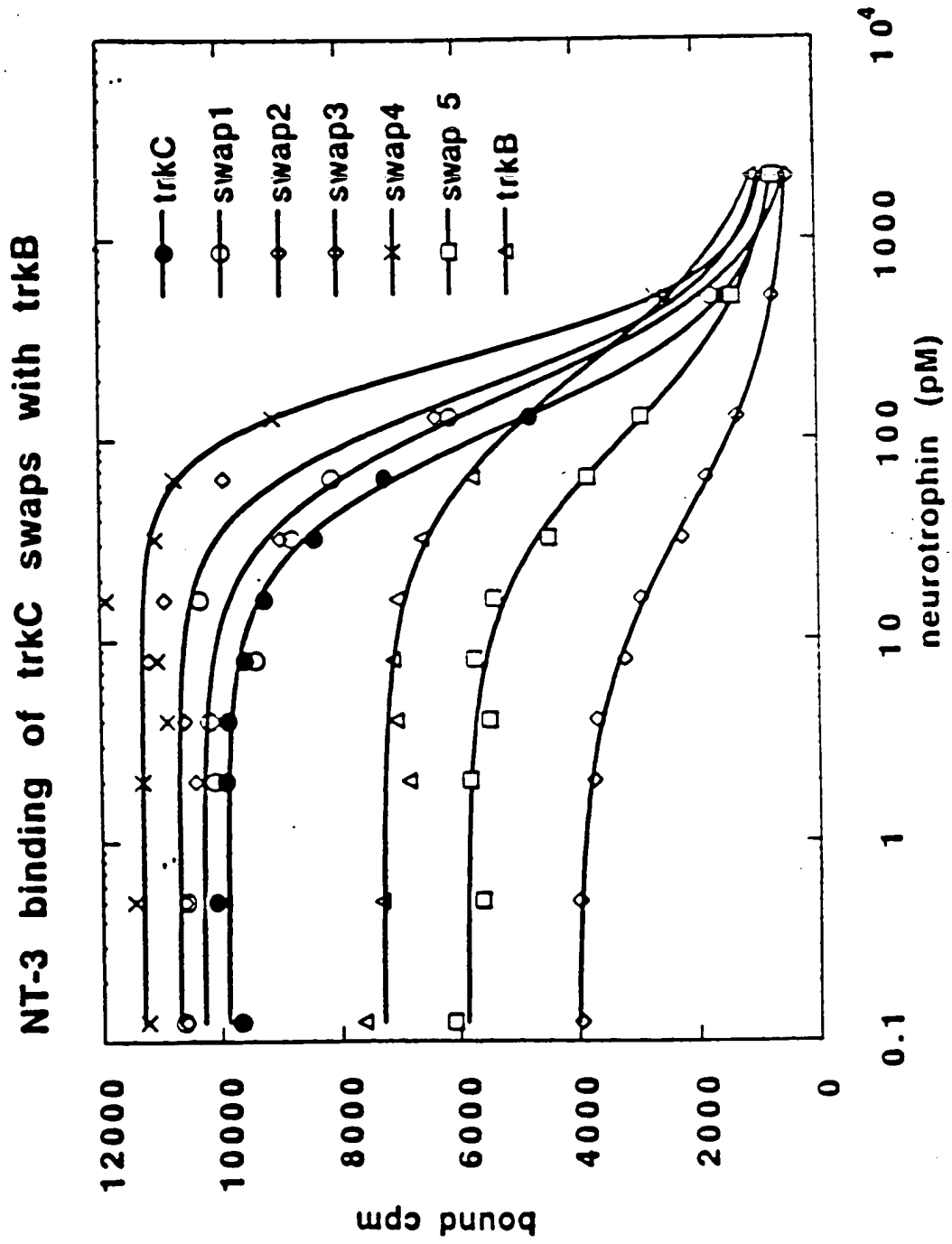
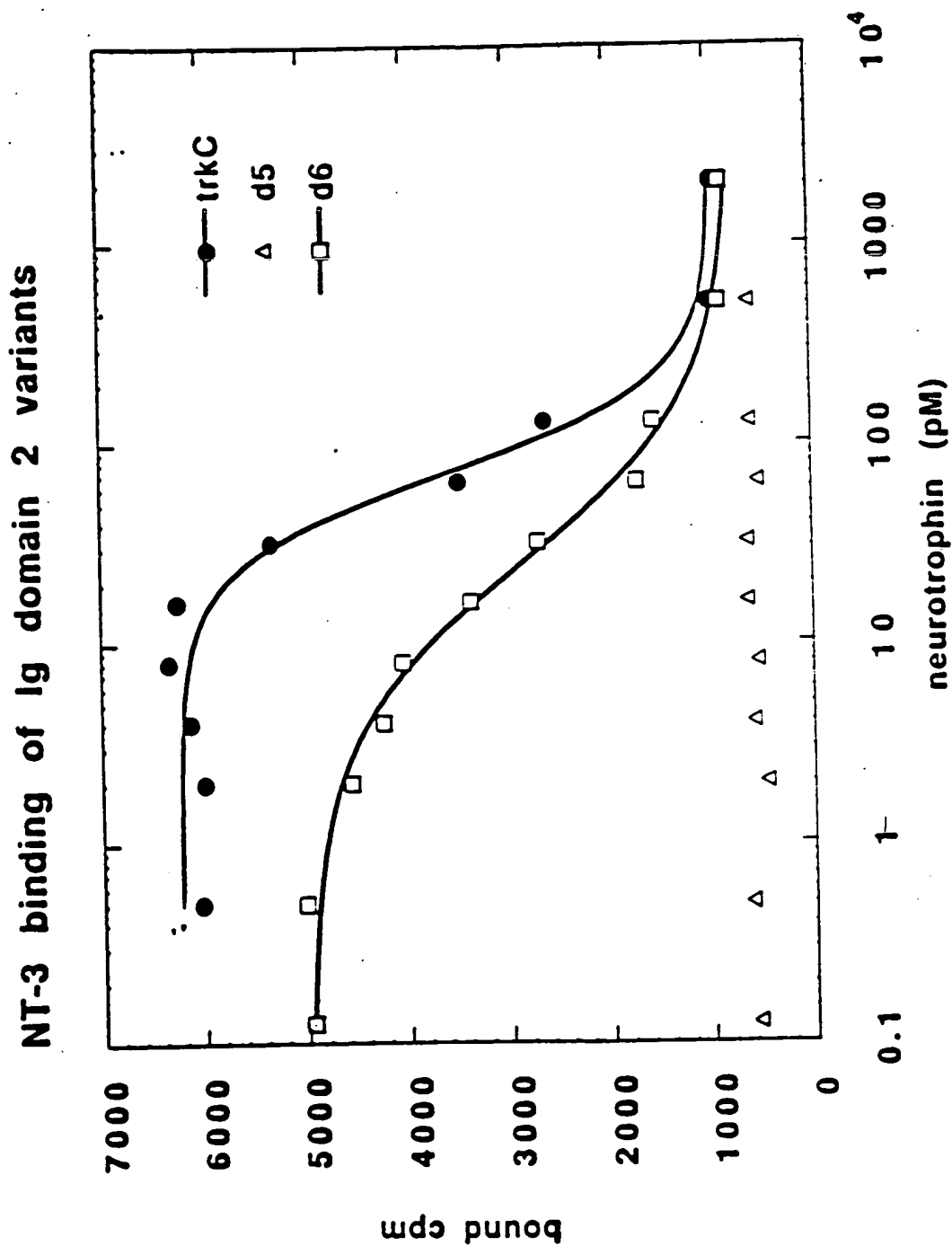


Figure 14c



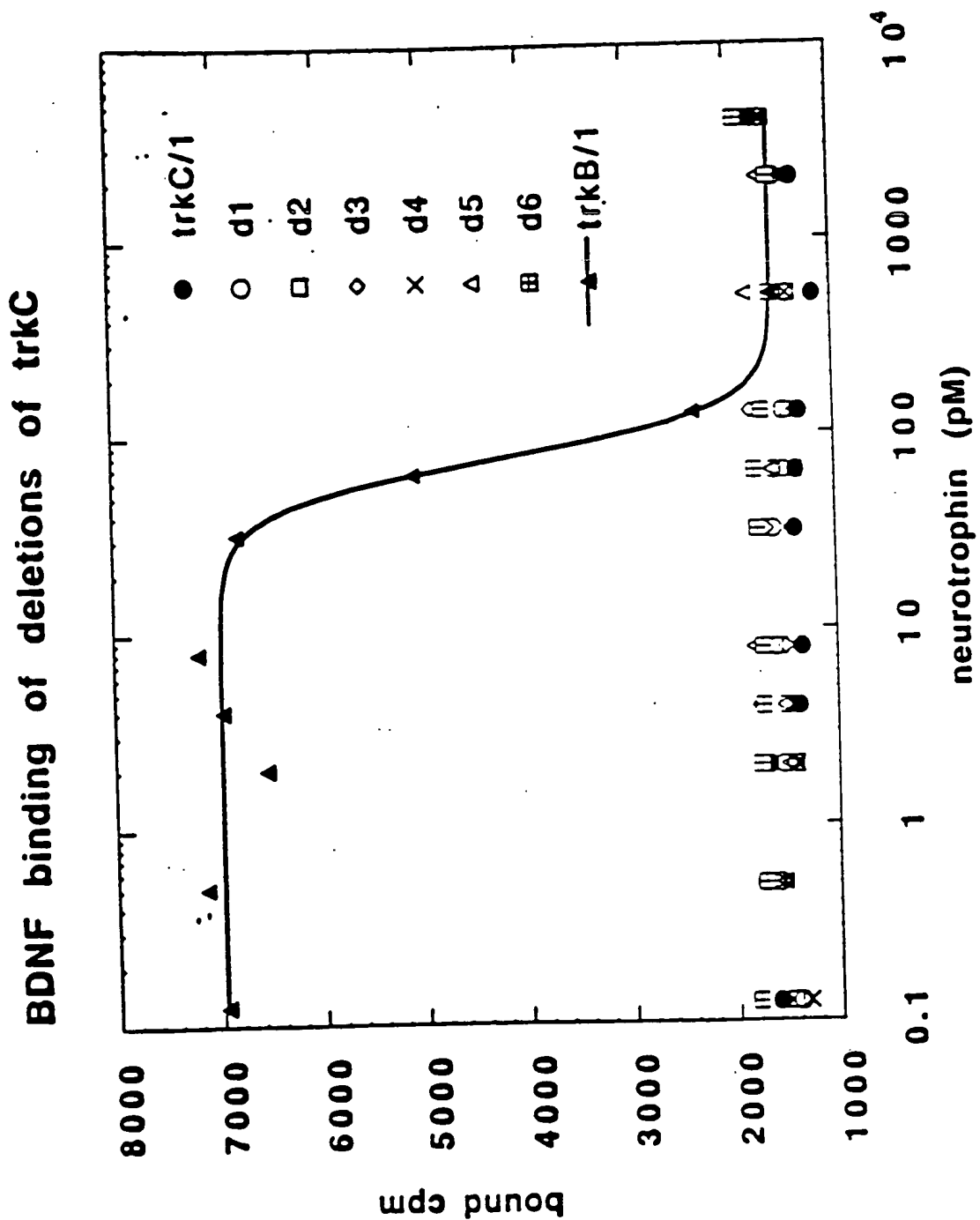
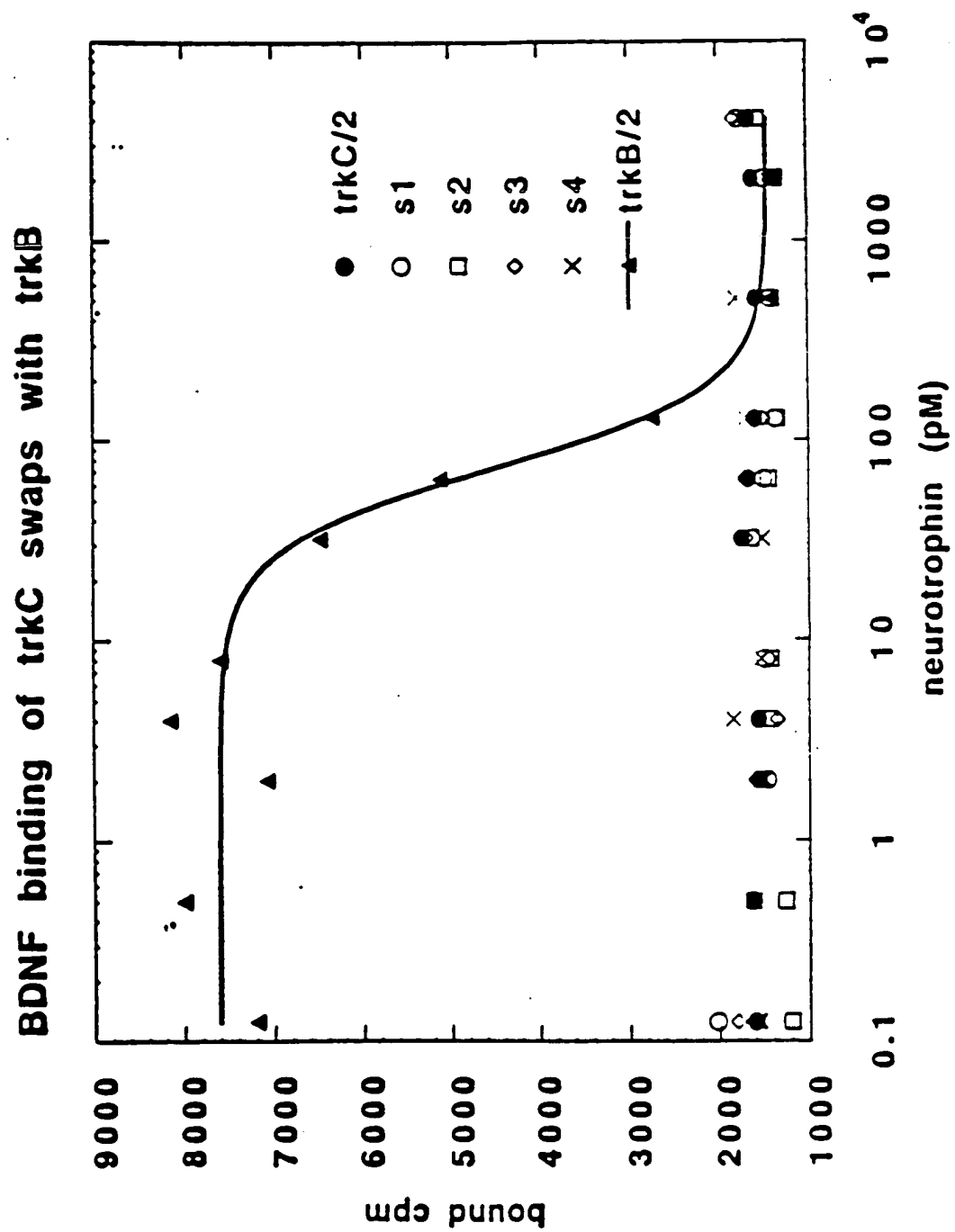
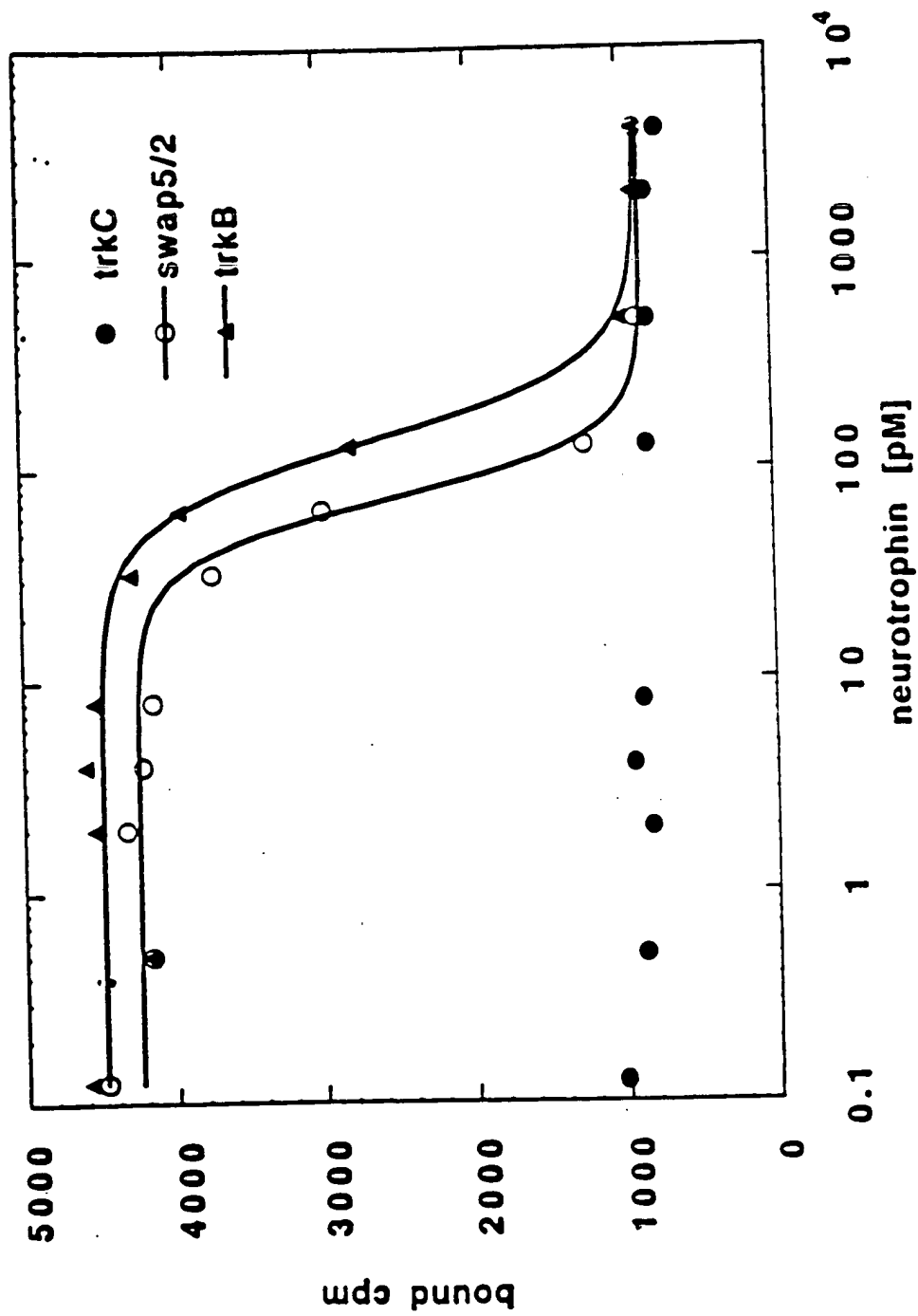


Figure 15A



BDNF binding of Ig domain 2 swap



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-----Signal-----Cysteine Rich I-----
trkA 1 MLRGRRGQLGWHSWAAGPGSLAWLILAS---AGAAACPDACCPHGSSGLRCTR-DGALDSLHMLPG---AENLTETIENHO
trkB 1 ---MSWIIRWHPAMARINGFCWLVVGFW---AAAFACPTS-CKCSASRIWCDSPSPGIVAFPALEPNVSD---PENLTETIANOK
trkC 1 ---MDVSL---CPAKCSFNRI-FLLGSWLDYVCSVLCPAN-CVCSKTEINCRPPDDGNL-FPLLEGQDSCHSNCHMANITDISAHTSIHIEWR

-----Leucine Rich-----Cysteine
trkA 78 HLQHLRLDLRLGLGELRLNLTIVKSGLRIVAPDAFHTTPRLSRNLNLSFNALESLSMTVOGLSLOELVLSGNPLHWCSCALRWLQRWEEELGCVPEQKLOC
trkB 78 RLIIINEDDVEAYVGLRNLTIVDSGLKIVAKKATLKNKLNQHNITRNKLTSLRKHFRHLDELSELIVGNPTFCSDIMWIKTLQE-AKSSPDQDLYC
trkC 90 SLHTLNAYDMELYTGLQKLTIKNSGLRSTQPAFAKNPHLYINLSSNRITLTSWOLFOTLSRELOLEQNFNCSDIRHMQLMQEOGEAKLNSQNYLC

Rich II-----Immunoglobulin I-----
trkA 178 HGQG---PLAHMPNASCGVPTLKVQVPNASVDVGDVLLRCQVEGRGLEQAGWILTELEQSATYHKS---GCLPSLGLTLANVTSDLNKKNLTCMAELN
trkB 177 LNESSKNIPLANLQTPNCGPSANLAAPNLTVEEGKSLTSCSVAGDPVPVHMVWDVGNLVSXHMNET---SHTQG-SLRITNISDDSGKQISCAENL
trkC 190 INADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNVITCNGSGSPLPDVDWIVTGLOSINTHOTNLNMTVHAINLTLVNVTSEDNGFTLTCAENV

-----Immunoglobulin II-----
trkA 271 VGRAEVSQVNVSPASVO-LHTAVEMHHNCIPFSDVCGPAPSLRWLFWGCVLNETSFITFELEPAANETVRHGCLRLNQPHTVNNQNTLLAAMPFGO
trkB 272 VGEDQDSVNLTVHFAPITITFLESPTSDHNCIPITVKGNPKPALQNTYNGAILNESKYICTKIH--VTNHTETNGCLQDNPHTMNNQDYYTLIAKNEYGK
trkC 290 VQMSNASVALTVYPPRVVSLLEPELRLNCIEFVVRGNPPPTLHNLKNGOPLRESKIIHVEYY--QEGEIS-EGCLLPKPTHYNNQNTLLIAKMPGCT

-----Transmembrane-----
trkA 370 ASASIMAAFM-----DNPF-----EF-NPEDPIPDNS-----TSGDPVEKKDET---FGVSVAVGLAVFACFLSTLLIVNKKCGRRNKFGIN
trkB 370 DEKQISAHFMGWPCTDDGANPNYPDVIYEDYCTAANDIGDTTNRSEIPSTDVTDKGTREHLSVAVVVIASVVGFC-LIVMLFLL-KLARHSHKFGMK
trkC 387 ANQTINGHFL-----KEPFEST-DNF-ILFDEVST-----PPITYTHKPED---FGVSIAGLAFAFVLLVVLVHINKYGRRSKFGMK

-----Juxta membrane-----
trkA 446 RP-AVLAPEDGLAMSLHMTLGGSSLSPTG-KGCSGLQG-----HIIENPOYF-----SDACVHHIKKADIVLKRELGECAFGRVFLAECNNLPEOD
trkB 446 GPASVISNDDDSASPLHHISNGSNTPSSEGGPDVAVIIGMTKIPVIEENPOYFGITNSQLKPDITVQHKKHINIVLKRELGECAFGRVFLAECNNLPEOD
trkC 446 GPVAVISGEEDSASPLHHINHGITTSSLDAGPDTVVIGMTKIPVIEENPOYFGITNSQLKPDITVQHKKHINIVLKRELGECAFGRVFLAECNNLPEOD

-----Tyrosine Kinase-----
trkA 532 KMLVAVKALKEASESARQDFOREAELLTMLOHQMIVRFVGVCTEGRPLLMVFETMRHGDINRFLRSHGPDAKLLAGGEDV-APGPGLGQLLAVASQVAA
trkB 566 KILVAVKTLKQASDNARKQFHREAEILLTNLQHEHIVKFGVCGVEDPLIMVFETMRHGDINRFLRSHGPDAMILVDCQPRQAKGELGSLQMLHIASQIAS
trkC 566 KMLVAVKALKOPTLAARKQFOREAEILLTNLQHEHIVKFGVCGGDDPLIMVFETMRHGDINRFLRSHGPDAMILVDCQPRQAKGELGSLQMLHIASQIAS

-----
trkA 631 GMVYLASQHFVHRDLATRNCLVGGGLVVKIGDFGMSRDVYSTDYRVGGHTMLPIRHMPPESILYRKFTTESDVNSFGVVLWEIFTYKQKPWQLSNTAE
trkB 663 GMVYLASQHFVHRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYRVGGHTMLPIRHMPPESIMYRKFTTESDVNSLGVVLWEIFTYKQKPWQLSNNVE
trkC 666 GMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYRVGGHTMLPIRHMPPESIMYRKFTTESDVNSFGVVLWEIFTYKQKPWQLSNTIEV

-----
trkA 731 IDCTTQGRELERPRACPEVYAIHRGCGWQREPOORHSIKDVHARLOALACAPPVYLDVLG
trkB 763 IECITQGRVLOAPRTCPQEVYELMGCGWQREPHMRKNIKGHTLLIONLAKSPVYLDILG
trkC 780 IECITQGRVLERPRVCPKEVYDVMGCGWQREPOORLNIKELYKILHARLOALATPIYLDILG

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Figure 16

Latency to Foot Withdrawal

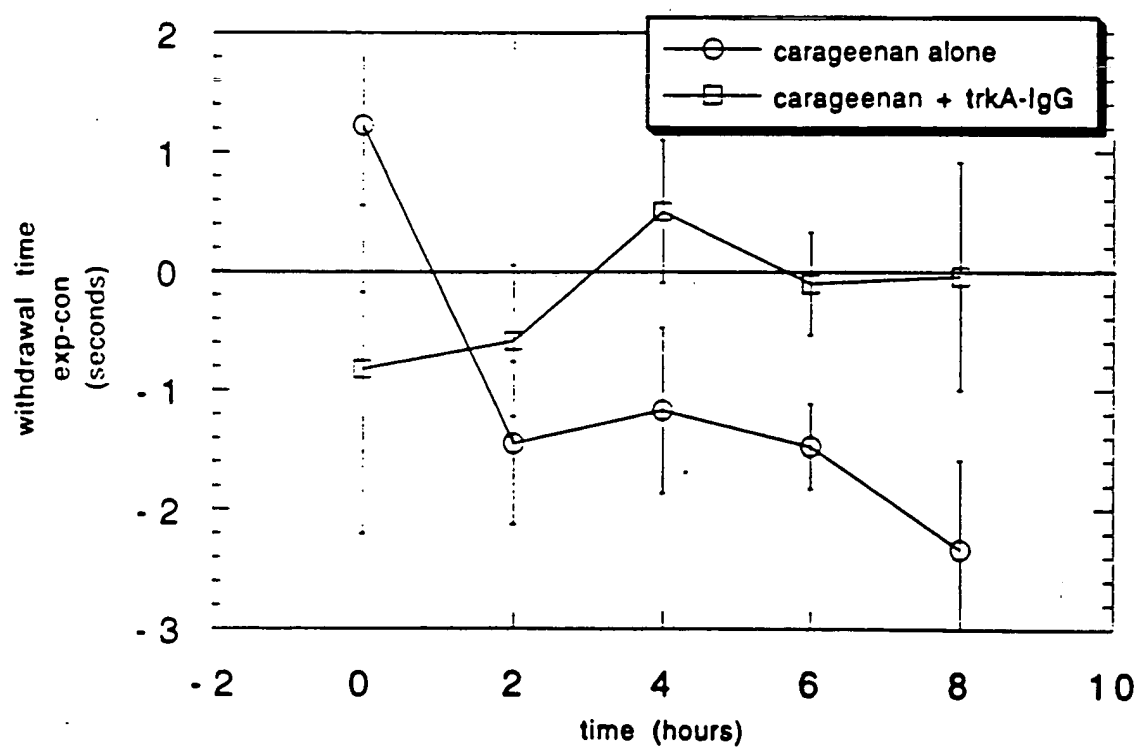


Figure 17

Latency to Foot Withdrawal

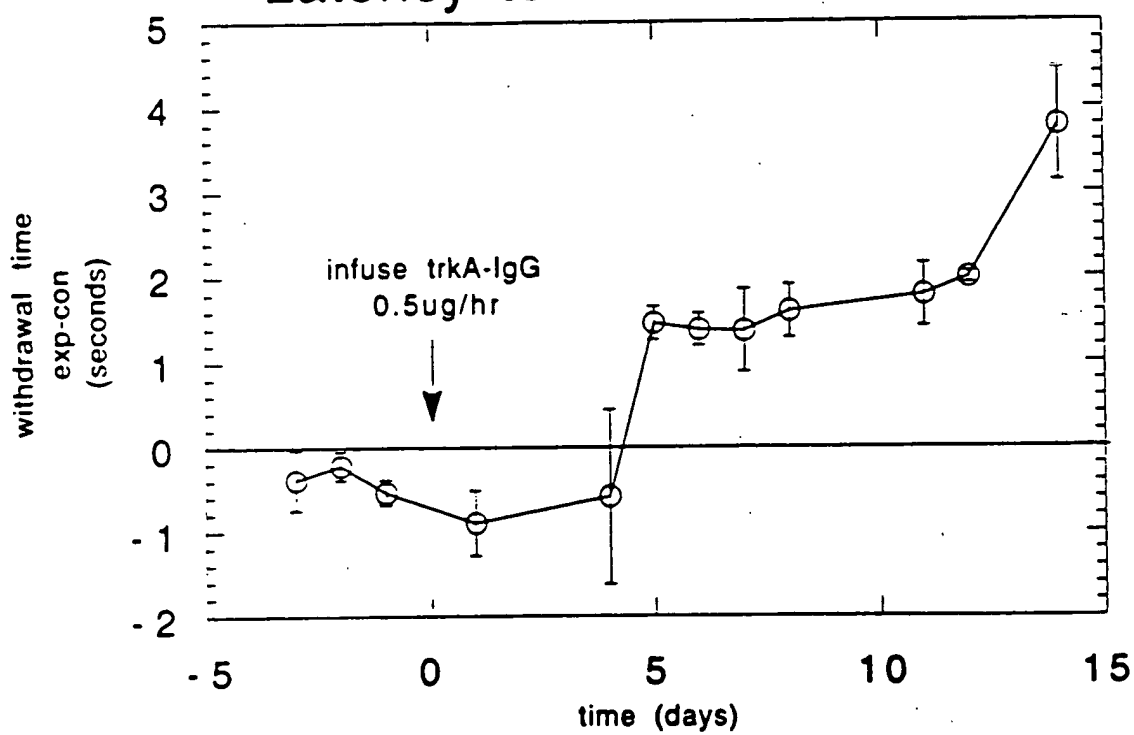


Figure 18